

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/217,780DATE: 04/08/94
TIME: 10:33:53

INPUT SET: S1916.raw

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This Raw Listing contains only the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

- (i) APPLICANT: Celeste, Anthony J.
Wozney, John
Rosen, Vicki A.
Wolfman, Neil
Thomsen, Gerald H.
Melton, Douglas A.

(ii) TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS

(iii) NUMBER OF SEQUENCES: 24

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: GENETICS INSTITUTE, INC.
- (B) STREET: 87 CambridgePark Drive
- (C) CITY: Cambridge
- (D) STATE: Massachusetts
- (E) COUNTRY: USA
- (F) ZIP: 02140

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US
- (B) FILING DATE:
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Lazar, Steven R.
- (B) REGISTRATION NUMBER: 32,618
- (C) REFERENCE/DOCKET NUMBER: 5202-CIP

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 617 876-1170
- (B) TELEFAX: 617 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

INPUT SET: S1916.raw

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47      (i) SEQUENCE CHARACTERISTICS:
48          (A) LENGTH: 926 base pairs
49          (B) TYPE: nucleic acid
50          (C) STRANDEDNESS: single
51          (D) TOPOLOGY: linear
52
53      (ii) MOLECULE TYPE: DNA (genomic)
54
55      (vi) ORIGINAL SOURCE:
56          (A) ORGANISM: Homo sapiens
57
58      (vii) IMMEDIATE SOURCE:
59          (B) CLONE: v1-1
60
61      (ix) FEATURE:
62          (A) NAME/KEY: mat_peptide
63          (B) LOCATION: 571..882
64
65      (ix) FEATURE:
66          (A) NAME/KEY: CDS
67          (B) LOCATION: 1..882
68
69
70      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
71
72      GCG CGT AAT ACG ACT CAC TAT AGG GCG AAT TGG GTA CGG GGC CCA GGC          48
73      Ala Arg Asn Thr Thr His Tyr Arg Ala Asn Trp Val Arg Gly Pro Gly
74      -190                      -185                      -180                      -175
75
76      AGC TGG ACT TCT CCG CCG TTG CTG CTG CTG TCC ACG TGC CCG GGC GCC          96
77      Ser Trp Thr Ser Pro Pro Leu Leu Leu Leu Ser Thr Cys Pro Gly Ala
78                      -170                      -165                      -160
79
80      GCC CGA GCG CCA CGC CTG CTG TAC TCG CGG GCA GCT GAG CCC CTA GTC          144
81      Ala Arg Ala Pro Arg Leu Leu Tyr Ser Arg Ala Ala Glu Pro Leu Val
82                      -155                      -150                      -145
83
84      GGT CAG CGC TGG GAG GCG TTC GAC GTG GCG GAC GCC ATG AGG CGC CAC          192
85      Gly Gln Arg Trp Glu Ala Phe Asp Val Ala Asp Ala Met Arg Arg His
86                      -140                      -135                      -130
87
88      CGT CGT GAA CCG CGC CCC CCC CGC GCG TTC TGC CTC TTG CTG CGC GCA          240
89      Arg Arg Glu Pro Arg Pro Pro Arg Ala Phe Cys Leu Leu Arg Ala
90      -125                      -120                      -115
91
92      GTG GCA GGC CCG GTG CCG AGC CCG TTG GCA CTG CGG CGA CTG GGC TTC          288
93      Val Ala Gly Pro Val Pro Ser Pro Leu Ala Leu Arg Arg Leu Gly Phe
94      -110                      -105                      -100                      -95
95
96      GGC TGG CCG GGC GGA GGG GGC TCT GCG GCA GAG GAG CGC GCG GTG CTA          336
97      Gly Trp Pro Gly Gly Gly Ser Ala Ala Glu Glu Arg Ala Val Leu
98                      -90                      -85                      -80
99

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100	GTC GTC TCC TCC CGC ACG CAG AGG AAA GAG AGC TTA TTC CGG GAG ATC	384
101	Val Val Ser Ser Arg Thr Gln Arg Lys Glu Ser Leu Phe Arg Glu Ile	
102	-75 -70 -65	
103		
104	CGC GCC CAG GCC CGC GCG CTC GGG GCC GCT CTG GCC TCA GAG CCG CTG	432
105	Arg Ala Gln Ala Arg Ala Leu Gly Ala Ala Leu Ala Ser Glu Pro Leu	
106	-60 -55 -50	
107		
108	CCC GAC CCA GGA ACC GGC ACC GCG TCG CCA AGG GCA GTC ATT GGC GGC	480
109	Pro Asp Pro Gly Thr Gly Thr Ala Ser Pro Arg Ala Val Ile Gly Gly	
110	-45 -40 -35	
111		
112	CGC AGA CGG AGG AGG ACG GCG TTG GCC GGG ACG CGG ACA GCG CAG GGC	528
113	Arg Arg Arg Arg Arg Thr Ala Leu Ala Gly Thr Arg Thr Ala Gln Gly	
114	-30 -25 -20 -15	
115		
116	AGC GGC GGG GGC GCG GGC CGG GGC CAC GGG CGC AGG GGC CGG AGC CGC	576
117	Ser Gly Gly Gly Ala Gly Arg Gly His Gly Arg Arg Gly Arg Ser Arg	
118	-10 -5 1	
119		
120	TGC AGC CGC AAG CCG TTG CAC GTG GAC TTC AAG GAG CTC GGC TGG GAC	624
121	Cys Ser Arg Lys Pro Leu His Val Asp Phe Lys Glu Leu Gly Trp Asp	
122	5 10 15	
123		
124	GAC TGG ATC ATC GCG CCG CTG GAC TAC GAG GCG TAC CAC TGC GAG GGC	672
125	Asp Trp Ile Ile Ala Pro Leu Asp Tyr Glu Ala Tyr His Cys Glu Gly	
126	20 25 30	
127		
128	CTT TGC GAC TTC CCT TTG CGT TCG CAC CTC GAG CCC ACC AAC CAT GCC	720
129	Leu Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala	
130	35 40 45 50	
131		
132	ATC ATT CAG ACG CTG CTC AAC TCC ATG GCA CCA GAC GCG GCG CCG GCC	768
133	Ile Ile Gln Thr Leu Leu Asn Ser Met Ala Pro Asp Ala Ala Pro Ala	
134	55 60 65	
135		
136	TCC TGC TGT GTG CCA GCG CGC CTC AGC CCC ATC AGC ATC CTC TAC ATC	816
137	Ser Cys Cys Val Pro Ala Arg Leu Ser Pro Ile Ser Ile Leu Tyr Ile	
138	70 75 80	
139		
140	GAC GCC GCC AAC AAC GTT GTC TAC AAG CAA TAC GAG GAC ATG GTG GTG	864
141	Asp Ala Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val	
142	85 90 95	
143		
144	GAG GCC TGC GGC TGC AGG TAGCGCGCGG GCCGGGGAGG GGGCAGCCAC	912
145	Glu Ala Cys Gly Cys Arg	
146	100	
147		
148	GCGGCCGAGG ATCC	926
149		
150		
151	(2) INFORMATION FOR SEQ ID NO:2:	
152		

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153      (i) SEQUENCE CHARACTERISTICS:
154          (A) LENGTH: 294 amino acids
155          (B) TYPE: amino acid
156          (D) TOPOLOGY: linear
157
158      (ii) MOLECULE TYPE: protein
159
160      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
161
162      Ala Arg Asn Thr Thr His Tyr Arg Ala Asn Trp Val Arg Gly Pro Gly
163      -190                      -185                      -180                      -175
164
165      Ser Trp Thr Ser Pro Pro Leu Leu Leu Leu Ser Thr Cys Pro Gly Ala
166                      -170                      -165                      -160
167
168      Ala Arg Ala Pro Arg Leu Leu Tyr Ser Arg Ala Ala Glu Pro Leu Val
169                      -155                      -150                      -145
170
171      Gly Gln Arg Trp Glu Ala Phe Asp Val Ala Asp Ala Met Arg Arg His
172                      -140                      -135                      -130
173
174      Arg Arg Glu Pro Arg Pro Pro Arg Ala Phe Cys Leu Leu Leu Arg Ala
175                      -125                      -120                      -115
176
177      Val Ala Gly Pro Val Pro Ser Pro Leu Ala Leu Arg Arg Leu Gly Phe
178                      -110                      -105                      -100                      -95
179
180      Gly Trp Pro Gly Gly Gly Gly Ser Ala Ala Glu Glu Arg Ala Val Leu
181                      -90                      -85                      -80
182
183      Val Val Ser Ser Arg Thr Gln Arg Lys Glu Ser Leu Phe Arg Glu Ile
184                      -75                      -70                      -65
185
186      Arg Ala Gln Ala Arg Ala Leu Gly Ala Ala Leu Ala Ser Glu Pro Leu
187                      -60                      -55                      -50
188
189      Pro Asp Pro Gly Thr Gly Thr Ala Ser Pro Arg Ala Val Ile Gly Gly
190                      -45                      -40                      -35
191
192      Arg Arg Arg Arg Arg Thr Ala Leu Ala Gly Thr Arg Thr Ala Gln Gly
193                      -30                      -25                      -20                      -15
194
195      Ser Gly Gly Gly Ala Gly Arg Gly His Gly Arg Arg Gly Arg Ser Arg
196                      -10                      -5                      1
197
198      Cys Ser Arg Lys Pro Leu His Val Asp Phe Lys Glu Leu Gly Trp Asp
199                      5                      10                      15
200
201      Asp Trp Ile Ile Ala Pro Leu Asp Tyr Glu Ala Tyr His Cys Glu Gly
202                      20                      25                      30
203
204      Leu Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala
205                      35                      40                      45                      50

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RAW SEQUENCE LISTING
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206
207 Ile Ile Gln Thr Leu Leu Asn Ser Met Ala Pro Asp Ala Ala Pro Ala
208 55 60 65
209
210 Ser Cys Cys Val Pro Ala Arg Leu Ser Pro Ile Ser Ile Leu Tyr Ile
211 70 75 80
212
213 Asp Ala Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val
214 85 90 95
215
216 Glu Ala Cys Gly Cys Arg
217 100
218

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: MP52

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 845..1204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

240
241
242 ACCGGGCGGC CCTGAACCCA AGCCAGGACA CCCTCCCCAA ACAAGGCAGG CTACAGCCCCG 60
243
244 GACTGTGACC CAAAAGGAC AGCTTCCCGG AGGCAAGGCA CCCCCAAAAG CAGGATCTGT 120
245
246 CCCCAGCTCC TTCCTGCTGA AGAAGGCCAG GGAGCCCGGG CCCCCACGAG AGCCCAAGGA 180
247
248 GCCGTTTCGC CCACCCCCCA TCACACCCA CGAGTACATG CTCTCGCTGT ACAGGACGCT 240
249
250 GTCCGATGCT GACAGAAAGG GAGGCAACAG CAGCGTGAAG TTGGAGGCTG GCCTGGCCAA 300
251
252 CACCATCACC AGCTTTATTG ACAAAGGGCA AGATGACCGA GGTCCCGTGG TCAGGAAGCA 360
253
254 GAGGTACGTG TTTGACATTA GTGCCCTGGA GAAGGATGGG CTGCTGGGGG CCGAGCTCCG 420
255
256 GATCTTGCGG AAGAAGCCCT CGGACACGGC CAAGCCAGCG GCCCCCGGAG GCGGGCGGGC 480
257
258 TGCCCAGCTG AAGCTGTCCA GCTGCCCCAG CGGCCGGCAG CCGGCCTCCT TGCTGGATGT 540

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/217,780

DATE: 04/08/94
TIME: 10:34:21

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Line	Error	Original Text
31	Wrong application Serial Number	(A) APPLICATION NUMBER: US

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PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION *US/08/217,780*

DATE: 04/08/94
TIME: 10:34:22

INPUT SET: S1916.raw

APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/08/217,780

DATE: 04/08/94
TIME: 10:34:22

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Line	Original Text	Corrected Text
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